AMENDMENTS TO THE CLAIMS

Claims 1 to 25 (cancelled)

Claim 26 (currently amended)

A single stranded oligonucleotide OY consisting of ~~having~~ 9 to 42 nucleotides of the sequence 9 to 42 nucleotides of the sequence Y_1-Y_2-Y_3-Y_4-Y_5 wherein Y_1 is a nucleotide sequence of 1 to 12 nucleotides or is hydrogen ~~suppressed~~, Y_2 is a trinucleotide which encodes for Gly, Y_3 is a nucleotide coding for Arg or Lys, Y_4 is a nucleotide coding for Arg or Lys and Y_5 is a nucleotide sequence, Y_6-Y_7-Y_8-Y_9 wherein Y_6 is a trinucleotide which codes for Ser, Thr or Tyr, Y_7 is a trinuucleotide which codes for any amino acid, Y_8 is a trinucleotide which codes for Glu or Asp and Y_9 is a nucleotide sequence of 1 to 12 nucleotides or Y_5 is ~~suppressed~~ hydrogen, with the exception of CGACACUCCA CCAUA.

Claim 27 (currently amended)

~~A~~ An oligonucleotide of claim ~~26~~ 2 wherein Y_1 and Y_9 are hydrogen.

Claim 28 (previously presented)

An oligonucleotide of claim 27 wherein Y_2 is a trinucleotide which codes for Gly, Y_3 is a trinucleotide which codes for Lys, Y_4 is a trinucleotide which codes for Arg and Y_5 is a sequence of 3 trinucleotides which code for Ser-Ala-glu.

Claim 29 (currently amended)

A single-stranded oligonucleotide OZ consisting of ~~having~~ 15 to 39 nucleotides and hybridizes under mild conditions with a consensus signal characteristic of amidated polypeptide hormones with the sequence having the formula

$$Z_1\text{-}Z_2\text{-}Z_3\text{-}Z_4\text{-}Z_5\text{-}Z_6\text{-}Z_7$$

wherein Z_1 is a nucleotide sequence of 1 to 12 nucleotide or is ~~suppressed~~ hydrogen, Z_2 and Z_3 are two trinucleotides which code for Leu, Z_4 and Z_5 are two trinucleotide which code for any two amino acids, Z_6 is a trinucleotide which codes for Leu and Z_7 is a nucleotide sequence of 1 to 12 nucleotides or its ~~suppressed~~ hydrogen.

Claims 30 to 32 (cancelled)

Claim 33 (new)

A method for identifying the non-amidified precursor of a peptide having an amidated C-terminal end comprising 1) obtaining a DNA sample, 2) amplifying the fragment of interest by PCR technique with a single stranded oligonucleotide OY consisting of 9 to 42 nucleotides of the sequence $Y_1\text{-}Y_2\text{-}Y_3\text{-}Y_4\text{-}Y_5$ wherein Y_1 is a nucleotide sequence of 1 to 12 nucleotides or is hydrogen, Y_2 is a trinucleotide which encodes for Gly, Y_3 is a nucleotide coding for Arg or Lys, Y_4 is a nucleotide coding for Arg or Lys and Y_5 is a nucleotide sequence,

Y_6-Y_7-Y_8-Y_9 wherein Y_6 is a trinucleotide which codes for Ser, Thr or Tyr, Y_7 is a trinucleotide which codes for any amino acid, Y_8 is a trinucleotide which codes for glu or Asp and Y_9 is a nucleotide sequence of 1 to 12 nucleotides or Y_5 is hydrogen.